**非非常有效的 计多分子 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人名英格兰 人名英格兰 人名英格兰 人姓氏格兰 人名英格兰 人名英格兰 人名英格兰 人名英格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人名英格兰 人名英格兰 人名英格兰 人姓氏格兰 人名英格兰 人名英格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人名英格兰 人名英格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人名英格兰 人名英格兰 人姓氏格兰 人名英格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰 人姓氏格兰 人名英格兰人姓氏格兰 人名英格兰 人名英格兰人姓氏格兰 人名英格兰人姓氏格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人姓氏格兰 人名英格姓氏格姓氏格姓氏格姓氏格姓氏格姓氏格姓氏格姓氏格姓氏格兰 人名英格兰人姓氏格兰 人名英格兰人姓氏格兰人姓氏格兰人姓氏格兰格姓氏格姓氏格兰格姓氏格姓氏格姓氏格兰格姓氏格姓氏格兰格姓氏格姓氏格姓氏格姓氏格姓氏格姓氏格姓氏格姓氏格姓氏格姓氏** (MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 09:23:39 2000; MasPar time 83.13 Seconds 16.486 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-09-331-631-1 (29-73) from US09331631.pep (2 of 5) 361

1 SEFDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYD 45

Scoring table: PAM 150 Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 34.353; Variance 52.501; scale 0.654

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

, 110,654 222 221 221 221 221	Result No.
115 101 101 102 95 95 97 77 77 77 77 77 77 77 77 77 77	Score
21. 22. 23. 24. 25. 26. 26. 26. 26. 26. 26. 27. 28. 20. 20. 20. 20. 20. 20. 20. 20. 20. 20	Query Match 1
588 605 1170 1170 1173 524 1172 1172 1170 1170 125 352 724 1170 726 128 1170 1172 1172 1172 1172 1172 1172 1172	Length
	B
VCLB_GOSHI VCLA_GOSHI AGRP_LUFCY TSP1_HUMAN TSP1_MOUSE TSP1_YENLA SBP_SOYBN TSP2_HUMAN TXR1_SCHPO CYSK_YEAST TSP2_BOVIN TSP2_BOVIN TSP1_HUMAN YORM_TTV1 ATI1_VACCV ATI1_CAMPC AGT1_CAMPC AGT1_CAMPC ATI1_COWPX TSP2_MOUSE ADO_HUMAN RRPO_ACLSA PUR6_PYROA Y107_METJA LAC1_NEUCR	ID
VICILIN C72 PRECURSOR VICILIN GC72-A PRECURS 6.5 KD ARGININE/GLUTAM 6.5 KD ARGININE/GLUTAM THROMBOSPONDIN 1 PRECU THROMBOSPONDIN 1 PRECU THROMBOSPONDIN 1 PRECU SUCROSE-BINDING PROTEI THROMBOSPONDIN 2 PRECU HYPOTHETICAL 49,6 KD P PUTATIVE CYSTEINE SYNT THROMBOSPONDIN 2 PRECU MAJOR EPIDIDYMIS-SPECI HYPOTHETICAL 38,6 KD P 94 KD A-TYPE INCLUSION PROTE UDP-N-ACETYLGLUGOSAMIN A-TYPE INCLUSION PROTE THROMBOSPONDIN 2 PRECU DP-N-ACETYLGLUGOSAMIN A-TYPE INCLUSION PROTE THROMBOSPONDIN 2 PRECU DP-N-ACETYLGLUGOSAMIN A-TYPE INCLUSION PROTE THROMBOSPONDIN 2 PRECU PHOSPHORIBOSYLAMINOIMI PHOSTHETICAL PROTEIN M HYPOTHETICAL PROTEIN M HACCASE PRECURSOR (EC	Description
2.20e-08 2.13e-05 2.13e-05 2.13e-05 2.13e-05 2.13e-06 2.00e-04 2.90e-04 3.08e-01 3.0	Pred. No.

밁

Query Match 31.9%; Best Local Similarity 31.7%; Matches 13; Conservative

Score 115; DB 1; Length 588; Pred. No. 2.20e-08; 13; Mismatches 12; Indels

ω

Gaps

Ψ

45	43	42	41	40	39	38	37	36	35	34	33	32	3 <u>1</u>	30	29	28	27	26	25	24
67	6 6 6 6 6 7 8 6 8	68	68	68	69	69	69	69	69	69	69	69	69	70	70	70	70	71	71	71
18.6	18.8	18.8	16.8	18.8	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.4	19.4	19.4	19.4	19.7	19.7	19.7
364	1711	674	646	383	2511	1106	741	427	382	363	348	139	<u>3</u> 3	1613	940	244	55	1336	702	619
<b>—</b> +		۲	<u>_</u>	Н	Н	$\vdash$	_	۰–۱	Н	$\vdash$	_	<u>_</u>	ш	ш	Н	Н	Ь	ப	ш	1
KITH_ILTVT	CHD1_MOUSE	DNLJ_THESC	SG1_BOVIN	D111_ARATH	FAS_CHICK	STC_DROME	FIBA_CHICK	YEBS_ECOLI	PTN2_MOUSE	PTN2_RAT	HM14_CAEEL	Z155_HUMAN	MBP1_MAIZE	VIT2_CAEEL	MAZ4_SCHCO	YL53_CAEEL	NXB2_CERLA	SEC3_YEAST	ATI1_VARV	LAC2_NEUCR
THYMIDINE KINASE (EC 2	CHROMODOMAIN-HELICASE-	DNA LIGASE (EC 6.5.1.2	SECRETOGRANIN I PRECUR	DNA-DAMAGE-REPAIR/TOLE	FATTY ACID SYNTHASE (E	SHUTTLE CRAFT PROTEIN.	FIBRINOGEN ALPHA/ALPHA	HYPOTHETICAL 48.3 KD P	PROTEIN-TYROSINE PHOSP	PROTEIN-TYROSINE PHOSP	HOMEOBOX PROTEIN CEH-1	ZINC FINGER PROTEIN 15	ANTIMICROBIAL PEPTIDE	VITELLOGENIN 2 PRECURS	MATING-TYPE PROTEIN A-	HYPOTHETICAL 29.0 KD P	NEUROTOXIN B-II.	EXOCYST COMPLEX COMPON	81 KD A-TYPE INCLUSION	LACCASE PRECURSOR (EC
1.19e+01	8.43e+00	8.43e+00	8.43e+00	8.43e+00	5.93e+00	5.93e+00	4.15e+00	4.15e+00	4.15e+00	4.15e+00	2.89e+00	2.89e+00	2.89e+00							

## ALIGNMENTS

DR DR SO	88888888	4888888	R R R R R R R R R R R R R R R R R R R	HERE SOOOD S	RESULT
 s; 1. al. VI	s SWISS-PROT entry is copyright. It is prod ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There by non-profit institutions as long as lifted and this statement is not removed. U ities requires a license agreement (See htt send an email to license@isb-sib.ch).	Plant Mol. Biol. 7:475-489(1986)	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Chlan C.A., Pyle J.B., Legocki A.B., Dure L. III;  Cherlopmental biochemistry of cottonseed embryogenesis and  germination. XVIII. cDNA and amino acid sequences of the members of the storage protein families.";	01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B). GOSSYPIUM hitsutum (Upland cotton). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.	LT 1 VCLB_GOSHI STANDARD; PRT; 588 AA. P09801:

Ş

32

DRQEYEECKRQCMQLETSGQMRR-CVSQCDKRFEEDIDWSK 71

```
RETERMENT
                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                            AGRP_LUF
P56568;
                          MEDLINE; 97357433.
Kimura M., Park S.S.,
Kimura M., etructure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 germination. XIX. Sequences and genomic of globulin (vicilin) genes of cottonseed."; plant Mol. Biol. 9:533-546(1987).
-i- FUNCTION: SEED STORAGE PROTEIN.
-i- SUBCELLULAR LOCATION: COTYLEDONARY MEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VICILIN GC72-A PRECURSOR (ALPHA-GLOBULN A).
Gossypium hirsutum (Upland cotton).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium
                                                                                                                          Luffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
 "Primary structure of the seeds of sponge Biosci. Biotechnol.
                                                         TISSUE-SEED MEDLINE; 97
                                                                                                                                                                                                 15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
Biosci.
                                                                                        SEQUENCE
                                                                                                                 Lutta.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M19378; AAA33069.1; PIR; S06398; S06398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chian C.A., Borroto K., Kamalay J.A., Dure L. III; "Developmental biochemistry of cottonseed embryogenesis germination. XIX. Sequences and genomic organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel.
01-MAR-1989 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P09799;
                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                   29
                                                                                                                                                                                   DEC-1998 (Rel. 37, Created)
DEC-1998 (Rel. 37, Last sequence update)
DEC-1998 (Rel. 37, Last annotation update)
EC-1998 (Rel. 37, Last annotation update)
KD ARGININE/GLUTAMATE-RICH POLYPEPTIDE (6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BODIES.
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONVICILIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              storage protein; s
                                                                                                                                                                                                                                                             LUFCY
                                                                                                                                                                                                                                                                                                                  SEFDRQE-YEECKRQCMQLETSGQM-R-RCVSQCDKRFEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _GOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00546; Seedstore_7s; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  24
605 AA;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                  71049 MW;
                                                                                                                                                                                                                                                                                                                                                                                       28.0%;
39.0%;
 . Sakai R., Yamasaki N., Funats of 6.5k-arginine/glutamate-rich gourd (Luffa cylindrica) "; Biochem. 61:984-988(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                         Score 101; DB 1;
Pred. No. 1.36e-05;
12; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                 VICILIN GC72-A.; C9DB9371C976953B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           605
                                                                                                                                                                                                                                                           47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                                           æ
                                            Funatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
                                                                                                                                                                                    .5K-AGRP).
                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                      Length 605;
                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                                                                                                          Indels
                            polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         γď
                                            G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gossypium
                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VICILIN
                             from
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                          4.
```

```
RESULT OF STREET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STARCCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. C
01-AUG-1988 (Rel. C
01-OCT-1996 (Rel. 3
THROMBOSPONDIN 1 PF
                                                                                         gene. DN.
                                                                                                                                                                                                                                                                          MEDLINE; 862
Dixit V.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSP1_HUMAN
P07996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
Submitted (XXX-1992) to
                                                                                                                                                                                                        Proc.
                                                                                                                                                                                                                                   "Characterization of a cDNA encoding the domains of human thrombosponding".
                                                                                                                                                                                                                                                                                                                                                                       analysis of proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hennessy S.W., Frazier B.A., Kim D.D., Baumgartel D.M., Rotvein P., Frazier W. "Complete thrombospondin mRNA sequence sites in the 3' untranslated region.", J. Cell Biol. 108:729-736(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multiple calcium-binding
proteins.";
                                                                                                                                             SEQUENCE OF 1-166 FROM N.A. MEDLINE; 89291870.
Laherty C.D., Glerman T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MASS SPECTRO
                                                                                         Laherty C.D., Glerman T.M., Dixit V.M.;
"Characterization of the promoter region
gene. DNA sequences within the first intr
J. Biol. Chem. 264:11222-11227(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                               Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-397
MEDLINE; 87157592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THBS1 OR TSP1 OR TSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seed storage
                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-374
                                                                                                                                                                                                                                                                                                                                                                                                            "Partial amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The structure of human thrombospondin, multiple calcium-binding sites and homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION:
                                                         SEQUENCE
                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawler
                                                                                                                                                                                                                                                                                                                                                      iochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSUE=ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \frac{\omega}{\omega}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESERVES DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTEYEACRVRCQVAEHGVERQRRCQQVCEKRLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQEYEECKRQCMQLETSGQM-RRCVSQCDKRFEE
                                                                                                                                                                                                                      ns of human thrombospondin. Natl. Acad. Sci. U.S.A. 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                       OF 1028-1170 FROM N
                                                                                                                                                                                                                                                                                               86287276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87057617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89139590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECTROMETRY:
                                                                                                                                                                                                                                                                                                                                                                                                                             S., Eden-Mccutchan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Metazoa; Chordata; Craniata;
Primates; Catarrhini; Hominid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hynes R.O.;
                                                                                                                                                                                                                                                                                                                                                                                       cDNA clones: homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-397 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
12 3
16 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                      25:8418-8425(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STORAGE PROTEIN WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103:1635-1648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOME, TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08, Created)
08, Last sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.7%;
41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GE PROTEIN WHICH PROVIDES NITROGEN GERMINATION AND SEEDLING GROWTH. RY: MW-5693.39; METHOD-MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \mathfrak{S}
                      ç
 Gauthier J., Kreis C.G. o the EMBL/GenBank/DDBJ GLYCOPROTEIN THAT MEDIA
                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                          F., Frams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEED STORAGE
                                                         Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           588B0EC82273AC05 CRC64;
                                                                                                                                                                                                                          83:5449-5453(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                             Framson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                                         to malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homologies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1170
                                                                                                           gion of intron
                                                                                                                                                                                                                                                                                                                                                                                       thrombospondin as determ: malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                               Rotwein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deckwerth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
12e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
 MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                          heparin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adhesive glycoprotein with ies with several different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                             the human
                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                             Bornstein
                      databases
                                                                                                                                                                                                                                                                             P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                         human thrombospondin rease transcription.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                            and
 CELL-TO-CELL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                               Frazier W.A.;
                                                                                                                                                                                                                                                            collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND CARBON
                                                                                                                                                                                                                                                                                                                                                                                                                                 ۳
:
                                                                                                                                                                                                                                                                                                                                                                                                            determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                            binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲
```

```
PROSITE; ...

PRAM; PF00008; EGF; 2.

PFAM; PF00093; tsp_1; 3.

PFAM; PF00093; vwc; 1.

PFAM; PF00093; Cell adhesion; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M25631; AAA36741.1; -
EMBL; X04665; CAA28370.1; -
EMBL; X14787; CAA32899.1; -
EMBL; J04835; AAA61178.1; -
EMBL; M99425; AAB59366.1; -
PIR; A05172; A05172.
PIR; A05172; A05172.
PIR; A25812, A25812.
PIR; A25815, A25815.
PIR; A30140; A30140.
PIR; A34274, A34274.
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                 REPEAT
REPEAT
REPEAT
DOMAIN
DOMAIN
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 1880
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; I
PIR; I
PIR; I
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGEN, FIBRONECTIN, LAMININ AND TYPE V COLLAGEN.
SUBUNIT: HOMOGRIMER, CROSS-LINKED BY DISULFIDE BONDS.
SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: CONTAINS 1 VWFC DOMAIN.
SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEAT (WHICH BIND CALCIUM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00022; EGF_1;
PS01186; EGF_2;
PS01208; VWFC; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1EMO
 FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . . . . . .
                                     TSP TYPE-1 1.

TSP TYPE-1 2.

TSP TYPE-1 3.

EGF-LIKE 1.

EGF-LIKE 2, CALCIUM-BINDING (POTENT EGF-LIKE 3.)

TSP TYPE-3 1.

TSP TYPE-3 3.

TSP TYPE-3 5.

TSP TYPE-3 5.

TSP TYPE-3 6.

TSP TYPE-3 7.

CELL ATTACHMENT SITE (POTENTIAL).

INTERCHAIN (PROBABLE).

INTERCHAIN (PROBABLE).

INTERCHAIN (PROBABLE).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                   3 X TSP TYPE REPEATS.
3 X EGF TYPE REPEATS.
7 X TSP TYPE-3 REPEATS.
C-TERMINAL.
-- TYPE-1 1.
 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calcium-binding; Heparin-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THROMBOSPONDIN :
                                                                                                                                                                                                                                                                                                                                                                                                                                               TSP TYPE-1 REPEATS (CS-LIKE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as
                                                                                                                                                                                                                                                                                                                                                                                                                    REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.
; (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    its content
                                                                                                                                                                                                                                                                                                                                                                                                                    (CA-BINDING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
TRESULT OF THE SECOND CONTROL OF THE SECOND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQ FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
 EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                   ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
```

```
Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSP1_MOUSE P35441;
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use: by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
THROMBOSPONDIN 1 PRECURSOR.
THBS1 OR TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bornstein P., Alfi D., Devarayalu S., Framson P., Li P., "Characterization of the mouse thrombospondin gene and evaluati the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16691-16698(1990).
-i- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-490 FROM MEDLINE; 90375546. Bornstein P., Alfi D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of mouse thrombospondin during cell growth and development."; J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92147683.
Laherty C.D., O'Rourke Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of the murine thrombospondin gene.";
Genomics 11:587-600(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawler J., Duquette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 SSVQTRTCHIQECDKRFKQDGGWS 439 : | | | | : : | | | | : | | | |
                                                                                                                                                                                                                                                                                                             LAMININ AND TYPE V COLLAGEN.
SUBGUST: HOMOTRIMER, CROSS-LINKED BY DISUL
SIMILARITY: BELONGS TO THE THROMBOSPONDIN
SIMILARITY: CONTAINS 1 VWFC DOMAIN.
SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS
(WHICH'BIND CALCIUM).
L; M62470; AAA50611.1;

M62450; AAA50611.1;

L; M62451; AAA50611.1;

L; M62452; AAA50611.1;

L; M62453; AAA50611.1;

L; M62453; AAA50611.1;

L; M62454; AAA50611.1;

L; M62455; AAA50611.1;

L; M62455; AAA50611.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSGQMRRC-VSQCDKRFEEDIDWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 26.3%;
Similarity 50.0%;
12; Conservative
                                                                                                                                                             s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92128941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1067
84
523
1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1067
84
523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ζ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ×
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ferro
 JOINED
JOINED
JOINED
JOINED
JOINED
JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 95;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
T -> A (IN REF. 2, 3
T -> A (IN REF. 2).
MW; 69B3EDE5AE3A395E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۳
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; L
1.90e-04;
                                                                                                                                                                                                                                                                                                                                                                                        BY DISULFIDE BONDS DSPONDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence and expression
                                                                                                                                                                                                                                                                                                                                   AND 7 TYPE-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seldin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d evaluation
.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                    TSP
                                                                                                                                                                                                                                                                             a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1:
                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                             outstation
                                                                                                                                                                                                                                                                                                                                    REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                       in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲,
```

Amphibia; Xenopodinae;

TYPE-3

TSP

REPEATS

FIBRONECTIN,

restrictions and

for

no 9 way

EMBL

Ø

collaboration - outstation outstation ä

```
Query Match
Best Local S
Matches 1
                                                                                                             DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                           REPEAT
SITE
                                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00090; tsp_1; 3. PFAM; PF00093; vwc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01022; EGF_1; PROSITE; PS01186; EGF_2; PROSITE; PS01208; VWFC; 1
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A40558; A40558.
B42587; B42587.
A37905; A37905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P35555;
                         Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain;
                                                                           926
270
270
2551
5551
5552
599
650
650
650
650
650
650
650
650
708
360
708
                       26.3%;
larity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA50611.
AAA50611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1EMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THBS1.
                                                                           Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
18
                                                                                    1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1170
232
373
548
690
950
1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adhesion;
                                                                                                                                                                                                                                           129646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOINED
JOINED
JOINED
JOINED
JOINED
JOINED
JOINED
JOINED
JOINED
JOINED
JOINED
JOINED
                                                                                                         INTERCHAIN (PODABLE).
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                       Score
Pred.
4; M
                                                                                                                                                                                                                                                                              TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 2. CA
EGF-LIKE 3.
TSP TYPE-3 1.
TSP TYPE-3 3.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 7.
TSP TYPE-3 7.
TSP TYPE-3 7.
TSP TYPE-3 7.
CELL ATTACHMEN
INTERCHAIN (PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 X TSP TYPE-1 REPEATS (CS-LIKE).
3 X TSP TYPE-3 REPEATS.
7 X TSP TYPE-3 REPEATS (CA-BINDIN C-TERMINAL.
                                                                                          POTENTIAL
F -> L (II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEPARIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THROMBOSPONDIN
                                                                                       ţ
                         Mismatches
                                                                          L (IN AAA53063)
0443£493615E7F06
                                   No. ;
                                                                                                                                                                                                                                                                                            ATTACHMENT SITE (POTENTIAL).
                                     DB 1; Le
1.90e-04;
                                                                                                                                                                                                                                                                                  (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                            CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEATS (CA-BINDING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                               Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heparin-binding; Repeat;
                                                                            CRC64;
                          Indels
                          ۳
                         Gaps
                          ۲,
                                                                                                                                                                                                                          RESULT

1 TSP1_XENLA
AC
P35448;
DT 01-JUN-1994 (
DT 01-OCT-196 (
DT 01-OCT-196 (
DT 01-OCT-1996 (
DE THROMBOSPOND)
GN THS51 OR TSP91 OS
ENARYOTA;
MARCHER SEQUENCE FROM
CC ELL-TO-1
CC INILARI
CC -!- SIMILARI
CC -!- SIMI
              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Urry L.A., Ramos J., Submitted (XXX-1993)
                       SITE
DISULFID
                                                 REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                   REPEAT
REPEAT
REPEAT
                                                                                                                                                                 REPEAT
                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00022; EGF_1; PROSITE; PS01186; EGF_2; PROSITE; PS01208; VWFC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS
-!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
-!- SIMILARITY: CONTAINS 1 VWFC DOMAINS.
-!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-
(WHICH BIND CALCIUM).
          DISULFID
                                                                                                                                        DOMAIN
                                                                                                                                                     DOMAIN
                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                             PFAM; PF00090;
PFAM; PF00093;
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L04278; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THROMBOSPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THBS1 OR TSP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416
                                                                                                                                                                                                                                                                                                                                 Lycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y L.A., Ramos J., Duquette M., Desimone D.W., Lawler J.;
mitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.
FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL
CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGGEN, FIBRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAMININ AND TYPE V COLLAGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSVQTRTCHIQECDKRFKQDGGWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSGOMRRC-VSQCDKRFEEDIDWS
                                                                                                                                                                                                                                                                                                                                                                                                                       P00740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laevis (African clawed
                                                                                                                                                                                                                                                                                                                     domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 (Rel. 29, Created)
4 (Rel. 29, Last segu
6 (Rel. 34, Last anno
NDIN 1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa; Chordata; Craniata; Ve: Anura; Mesobatrachia; Pipoidea;
78824
5584
5584
5584
5584
5584
5584
5584
                                                                                                               382
438
438
550
550
762
762
                                                                                                                                                                                                                                                                                                                                                                                                                          1IXA
                                                                                                                                                                                                                                                                                                                                    Cell
                                                                                                                                                                                                                                                                                                                                               tsp_1;
                                                                                                                                                                                                                                                                                                                                                                        EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                    Signal.
                                      494
590
590
648
693
761
784
784
820
820
820
820
820
821
931
                                                                                                                                                                                                                                                                                                                                   adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                             FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update) annotation updat
         3 X TSP TYPE-1 REPEATS (CS-LIKE).
3 X EGF-TYPE REPEATS.
7 X TSP TYPE-3 REPEATS (CA-BINDING)
C-TERMINAL.
TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 3.
TSP TYPE-3 2.
TSP TYPE-3 2.
TSP TYPE-3 3.
TSP TYPE-3 4.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 7.
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                              POTENTIAL.
THROMBOSPONDIN 1
HEPARIN-BINDING
                                                                                                                                                                                                                                                                                                                                Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata;
ea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ŗ
                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                 Heparin-binding; Repeat;
```

(CA-BINDING).

(POTENTIAL)

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA Grimes H.D., Overvoorde P.J., Ripp K., Franceschi V.R., Hitz W.D.;

RT 18-62-kD sucrose binding protein is expressed and localized in

RI tissues actively engaged in sucrose transport.";

RI Plant Cell 4:1561-1574(1992).

C -!- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.

C -!- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.

C -!- TISSUE SPECIFICITY: ASSOCIATED MITH THE PLASMA MEMBRANE OF

C SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE

C SEVERAL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF

C MATURE PHLOEM AND THE CELLS OF EVELOPING COTYLEDONS.

C MATURE PHLOEM AND THE COTYLEDON, EXPRESSION IS NOT DETECTED

C MATURE OF SUCROSE IN THE COTYLEDON, EXPRESSION IS NOT DETECTED

C UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER

C FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30

C DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO

EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS THE

C RATE OF SUCROSE UPTAKE IN THE COTYLEDON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
EMBL; L06038; AAB03894.1; -.
PIR; J01730; J01730.
HSSP; P50477; ICAW.
PFAM; PF00546; Seedstore_7s; 1
Transport; Sugar transport; Si
SIGNAL 1 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                             This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Strepto
euphyllophytes; Spermatophyta; Ma
core eudicots; Rosidae; eurosids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SBP_SOYBN STANDARD; PRT; 524 AA Q04672; O1-JUN-1994 (Rel. 29, Created) O1-JUN-1994 (Rel. 29, Last sequence update) O1-JUN-1994 (Rel. 29, Last annotation updat SUCROSE-BINDING PROTEIN PRECURSOR (SBP).
                                                                                                                                                    or send
                                                                                                                                                                                                 modified and
                                                                                                                                                                                                                       use
                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
                                                                                                                                                                                            European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSGQMRRC-VSQCDKRFEEDIDWS
                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSVQTRSCQIQDCDKRFKQDGGWS
                                                                                                                                                        an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 26.0%;
Similarity 50.0%;
12; Conservative
                                                                                                                                                                      non-profit instituend this statement requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93104680.
                                                                                                                                                    equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1070
1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578
595
602
662
663
660
661
158
158
158
158
158
158
158
158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589
611
620
647
666
679
692
1158
1158
1250
250
363
705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptophyta; Embryophyta; Tracheophyta;
hyta; Magnoliophyta; eudicotyledons;
urosids I; Fabales; Fabaceae; Papilionoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                      Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARI
BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           re 94; DB 1; I
d. No. 2.94e-04;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A9F036D6516C0F24 CRC64;
                          Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524 AA
                                                                                                                                                                        (See http://www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1173;
                                                                                                                                                                        y and fo
.isb-sib.
                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۳.
                                                                                                                                                                                                 for
                                                                                                                                                                          ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                            in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲,
```

```
THE WE REAL COORDINATE OF THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P35442;
01-JUN-1994 (Rel.:
01-JUN-1994 (Rel.:
15-JUL-1999 (Rel.:
THROMBOSPONDIN 2 PI
THBS2 OR TSP2.
                                                  PFAM; PF00090; tsp_1; 3.
PFAM; PF00090; vsc; 1.
Glycoprotein; Cell adhesion; EGE-like domain: simm?
                                                                                                                                              PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                            PIR: A42173; A42173.
HSSP; P00740: 1IXA.
MIK: 188061;
                 SIGNAL CHAIN
                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
SEQUENCE
                                                                                                                                                                                                                                                          EMBL; L12350;
EMBL; M81339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSP2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Labell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Labell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 CKRQCMQLE--TSGQMRRCVSQCDKRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 CKHQCQQQQQYTEGDKRVCLQSCD-RY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISUI
SIMILARITY: BELONGS TO THE THROMBOSPONDIN
SIMILARITY: CONTAINS 1 VWFC DOMAIN.
SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WHICH BIND CALCIUM)
                                                                                                                                                                                                                                                                             L12350; AAA03703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potential regulatory ics 17:225-229(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T.L., McGookey Milewicz D. bospondin II: partial cDNA sion of a second member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.L., Byers P
                                                                                                                                            ; PS00022; EGF_1;
; PS01186; EGF_2;
; PS01208; VWFC; 1
e domain; Signal.
1 18
19 1172
19 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94010892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92217961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF 560-1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29,
38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              524
60522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .н.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                   FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 77; I
                                                                       Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUCROSE-BINDING PROTEIN. 0251EE90796EF341 CRC64;
THROMBOSPONDIN 2. HEPARIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.J., Disteche C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence, chromosome location, the thrombospondin gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      he complete human thrombospondin the 3' untranslated region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
3.08e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND
                                                                       Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Byers P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE-3
                                                                                                                                                                                                                                                                                                                                   .isb-sib
                                                                                                                                                                                                                                                                                                                                                                                       restrictions
                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                             Igh a o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
                                                                                                                                                                                                                                                                                                                                   .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                             outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
in
                                                                                                                                                                                                                                                                                                                                                                        no
                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
```

```
RESULTING
                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                  Q10223;
01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
01-OCTHETICAL 49.6 K
       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement or send an email.
                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                         Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
                                                                                                                                                                                               YAZ1
                                                   between
                                                                                           STRAIN-972;
                                                                                                     SEQUENCE
                                                                                                                    Schizosaccharomycetaceae;
                                                                                                                                             SPAC13D6.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                       416 LGPSIQTRACSLSKCDTRIRQDGGWS 441
                                                                                                                                                                                                                                                                                                                                                                                                                 ISULFID
                                                                                                                                                                                                                               46
                                                SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                             SCHPO
                                                                                                                                                                                                                               LETSGOMRRC-VSQCDKRFEEDIDWS
                                                                                                                                                                                                                                                               Similarity
12; Conser
                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                5549
6488
7761
7761
7761
7864
8843
8843
9917
7864
6553
5577
6552
7666
7584
7584
                                                                                                                                                    (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
L 49.6 KD PROTEIN C13D6.01 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318
381
549
725
953
381
437
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                AA,
                                                                                                                                                                                                                                                                                                         1069
                                                                                                                                                                                                                                                                                                                21.3%;
                                                                                                                                                                                                                                                                                                129955
                                                                                                                    Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENT EGF-LIKE 3.
TSP TYPE-3 1.
TSP TYPE-3 2.
TSP TYPE-3 3.
TSP TYPE-3 4.
TSP TYPE-3 6.
TSP TYPE-3 6.
TSP TYPE-3 7.
TSP TYPE-3 7.
TSP TYPE-3 7.
TSP TYPE-3 7.
CELL ATTACHMENT SITE (POTENTIAL).
INTERCHAIN (PROBABLE).
                                                                                                                                                                                                                                                             Score 77;
Pred. No.
3; Misma
                                                                                                                                                                                                                                                                                                             INTERCHAIN (PROBABLE).
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 X TSP TYPI
3 X EGF-TYPI
7 X TSP TYPI
C-TERMINAL.
                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSP TYPE-1 REPEATS (CS-LIKE).
EGF-TYPE REPEATS.
TSP TYPE-3 REPEATS (CA-BINDING)
                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                2AC7BB230E44C6F5 CRC64;
                                                                                                                                                                                                                                                                      77; DB 1;
No. 3.08e-01
                                                                                                                                                                                             431 AA.
               (See http://www.isb-sib.ch/announce/
                             There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALCIUM-BINDING (POTENTIAL).
                       Usage
                                                                                                                                                                                                                                                                              Length 1172
                         γď
                                        restrictions
                         and
                                                  EMBL
                                                                                  Walsh
                    is
                                                          ø
                                                                                                                                                                                                                                                               ۳.
                                                   collaboration -
                                  in
                                                                                  S.V.;
                                                                                                                                                                                                                                                               Gaps
                        in no way commercial
                                         og.
                                                                                                                                                                                                                                                               ۲
, V
                                                                                                   망
                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
(CISP).
```

Ş 8

```
SQ
                                                                                                                                                                                                 Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 1
TSP2_BOVIN STAN
Q95116; 01-NOV-1997 (Rel. 3
15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
THROMBOSPONDIN 2 PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYSK_YEAST
P53206;
01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z69725;
Hypothetical p
SEQUENCE 431
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
PUTATIVE CYSTEINE SYNTHASE (EC 4.2.99.8) (O-ACETYLSERINE SULFHYDRYLASE) (C-ACETYLSERINE (THIOL)-LYASE) (CSASE).
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                     EMBL; 272797; PROSITE; PS009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- PATHWAY: CYSTEINE BIOSYNTHESIS
                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                         Hypothetical protein; Lyase;
                                                                                                                                                                                                                                                                                                                        PFAM; PF00291; S_T_dehydratase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                                                      Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast 13:1077-1090(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGR012W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rieger M., Brueckner M.,
                                                                                                                                                                     167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence analysis
                                                                                                                                        32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 FKPQTFDEFV-HCLA-RVRA-MKRLVSICSN-FDEEDNWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: CYSTEINE BIOSYNTHESIS. SIMILARITY: BELONGS TO THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETATE
                                                                                                                                      DRQEY-EECKRQCMQLETSGQMRRCVSQCDKRFEEDIDW
                                                                                                                                                                    DPNQYVNAAKKACNELKKSGNGIRAVFA-D-QFENEANW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDIDWS
                                                                                                                                                                                                Similarity 33.3%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 20.8%;
Similarity 30.0%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                      PS0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97435481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al protein
431 AA; '
                                                                                                                                                                                                                                                             393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                   CAA96995.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAA93541.1;
                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                       1; CYS_SYNTHASE; 1.
. 35, Created)
. 38, Last sequence update)
. 38, Last annotation update)
PRECURSOR (CORTICOTROPIN-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 203
                                                                                                                                                                                                               20.5%;
                                                                                                                                                                                                                                                           42801 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces.
                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O-ACETYL-L-SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schaefer M.
3 kilobases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                Score
Pred.
8; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                         PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                         Cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetes;
                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                           76C73396D77B69AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132FB0919646AC9F CRC64;
                                                                                                                                                                                                re 74; DB 1; 1
d. No. 9.59e-01
Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from
                                                                            1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mueller-Auer S.;
rom Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                                     biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHASE/CYSTATHIONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .59e-0
                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               +
                                                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H(2)S
                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                        69
                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 431;
                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
    SECRETED
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
ent is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL
    PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration - MRL outstation
                                                                                                                                                                                                 ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                              tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                          outstation
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                   ų.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
```

```
REPEAT
REPEAT
REPEAT
REPEAT
SITE
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domaine in adrenocortical cells.",

J. Cell. Physiol. 167:164-172(1996).

-i- function: Adhesive Glycoprotein That Mediates Cell-to-cell and Cell-to-matrix interactions. Can bind to fibringen, fibronectin, Laminin and Type v Collagen.

-i- subunit: Homotrimer, Cross-linked by Disulfide Bonds.
-i- subunit: Belongs to the Thrombospondin family.
-i- similarity: Contains 1 vwfc Domain.
-i- similarity: Contains 3 egf-like Domains.
-i- similarity: Contains 3 type-1 tsp repeats and 7 type-3 tsp repeats (which bind Calcium).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00022; EGF_1; PROSITE; PS01186; EGF_2; PROSITE; PS01208; VWFC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00090; tsp_1; 3. PFAM; PF00093; vvc; 1. Glycoprotein; Cell adhesion; EGF-like domain; Signal.
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted protein/thrombospondin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-522 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penhoat A., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lafeuillade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THBS2 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Opposite regulation of thrombospondin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X96540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAR-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAA65385.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pellerin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
    1170
2332
5475
5475
5490
1170
6430
1430
1430
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
15491
154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lafeuillade M., Keramidas
, Mosher D., Chambaz E.M.,
) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ı s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FALSE_NEG
                                                                          TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENT EGF-LIKE 3.
TSP TYPE-3 1.
TSP TYPE-3 2.
TSP TYPE-3 4.
TSP TYPE-3 5.
TSP TYPE-3 6.
TSP TYPE-3 6.
TSP TYPE-3 6.
TSP TYPE-3 7.
CELL ATTACHMENT SITE (POTENTIAL).
INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
INTERCHAIN (PROBY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                      TSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keramidas M.,
                                                                                                                                                                                                                                                                                                                                                                                                               C-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEPARIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THROMBOSPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  ×××
                                                                                                                                                                                                                                                                                                                                                                                                                              TSP TYPE-1 REPEATS
EGF-TYPE REPEATS.
TSP TYPE-3 REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ondin-1 and corticotropin-induced expression by adrenocorticotropi
                                                                                                                                                                                                                                                                                                                                                32 H
                                                                                                                                                                                                                                                                                                          CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Danik M.,
                                                                                                                                                                                                                                                                                                                                                                                                                            REPEATS (CA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heparin-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M., Aguesse-Germon
Feige J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenocorticotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CS-LIKE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chambaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ß
```

```
THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                       CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP4_HUMAN STANDARD: PRT; 1
014508; 015-7UL-1998 (Rel. 36, Created)
15-7UL-1998 (Rel. 36, Last sequence up
15-FEB-2000 (Rel. 39, Last annotation
MADOR EPIDIDYMIS-SPECIFIC PROTEIN E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                               Signal; Glycoprotein
SIGNAL 1
                                                                                                                                                                                                   PROSITE; PS00317; 4_DISULFIDE_CORE; PFAM; PF00095; wap; 2.
                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence homology to extracellular proteinase inhib Biol. Reprod. 45:350-357(1991).
-!- FUNCTION: POSSIBLE FUNCTION IN SPERM MATURATION
                                                                                                           DOMAIN
                                                                                                                                               CHAIN
                                                                                                                                                                                                                                       EMBL; A18924; CAA01433.1; HSSP; P19957; 1FLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
-i- TISSUE SPECIFICITY: EPITHELLAL CELLS OF THE EPIDIDYMAL PREDOMINANTLY WITHIN THE DISTAL SECTIONS.
-i- SIMILARITY: TO WAP-TYPE 'FOUR-DISULFIDE CORE' PROTEINS.
                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                           EMBL; X63187; CAA44869.1; -.
                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92153963.
Kirchhoff C., Habben L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-EPIDIDYMIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECRETORY PROTEIN E4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 LGPSIQTRACSLGRCDHRIRQDGGWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 LETSGQMRRC-VSQCDKRFEEDIDWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%;
Similarity 42.3%;
11; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    f C., Habben L., Ivell R., human epididymis-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       936
1067
1170
                                                                         125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            599
620
650
657
678
151
151
316
330
455
582
                                                                                            1
22
27
76
44
   Conservative
                                                                         Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        936
1067
                                                                                                          21
125
75
125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617
644
663
676
689
151
151
316
330
455
582
                  20.2%;
                                                                       44
13136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129862
                                                                                                                                                                                                                                                    .'
                                                                         WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t annotation update)
PROTEIN E4 PRECURSOR (HE4) (EPIDIDYMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74; D
Pred. No. 9.
5; Mismatc
Score 73;
Pred. No.
7; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W.
                                                                      N-LINKED (GLCNAC. . .) (P
; B5BF5C08FF70E245 CRC64;
                                                                                                          POTENTIAL.

MAJOR EPIDIDYMIS-SPECIFIC

WAP 1.

WAP 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
W; 9CF1FBF55B89A051 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata;
 re 73; DB 1; Lod. No. 1.39e+00; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krull N.;
CDNA encodes a protein with roteinase inhibitors.";
                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
                                                                                                                                                                                                                                                                                                                                noved. Usage by and fo
(See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; I
9.59e-01;
                                                                                                                                                                                                                                                                                                                                                                  There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                     Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1170;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                   restrictions
                                                                                                                                               PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL
                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUCT,
 ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲
                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                  .ch/announce,
                                                                                                                                                                                                                                                                                                                                                                    'n
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                               , o
                                                                                                                                                                                                                                                                                                                                                                    no
 ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
```

밁

94

117

```
FRESULT RESULT R
                    RESULT
ID A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HYPOTHETICAL 38.6 KD PROTEIN.
Thermoproteus tenax virus 1 (strain KRA1) (TTV1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YORM_TTV1
P19297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 14
ACCV STANDARD; PRT; 724 AA. 4711 VACCV STANDARD;
P24759;
Ol-MAR-1992 (Rel. 21, Created)
Ol-MAR-1992 (Rel. 21, Last sequence update)
Ol-JUL-1993 (Rel. 26, Last annotation update)
94 KD A-TYPE INCLUSION PROTEIN (ATI).
"Isolation and characterization of modified 94-kDa inclusion protein. Virology 185:768-778(1991).
                                                                                      MEDLINE; 92074241.
de Carlos A., Paez E.;
                                                                                                                SEQUENCE FROM N.A. MEDLINE; 92074241.
                                                                                                                                                                                                                                          Amegadzie B.Y., Sisler Frame-shift mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 91310644.
Amegadzie B.Y., Ahn B.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccinia virus (strain WR)
Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                              Virology
                                                                                                                                                                                                                     protein gene.
                                                                                                                                                                                                                                                                                                                                                                                               35,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X14855; CAA32993.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoproteus tenax virus Viruses, dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                       Manegadzie B.Y., Ahn B.-Y., Moss B.;
"Identification, sequence, and expression of the gene encoding a M
35,000 subunit of the vaccinia virus DNA-dependent RNA polymerase.
J. Biol. Chem. 266:13712-13718(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279
                                                                                                                                                                                                                                                                                                                      EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pothrixvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRDQCQVDTQCPGQMKCCRNGCGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRQEYEECKRQCMQLETSGQMRRCVSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTQAFQQCISSCYQ-QTSGRTQ-CINNC: | :::| | :|||: |:: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKRQC-MQLETSGQMRRCVSQCDK
                                                                                                                                                                                              186:777-782(1992).
                                                                                                                                                                                                                                                                                              92124754
                                                                                                                                                                                                                                                                                                                         FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ai protein.
352 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%;
larity 32.1%;
Conservative
                                                                                                                                                                                                                                                                                                                         N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38674 MW;
                                                                                                                                                                                                                                             c J.R., N
s within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          no RNA stage; Lipothrixviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; DB 1; I
Pred. No. 1.39e+00;
9; Mismatches 8
                                                                                                                                                                                                                                             Moss
n the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0D0E49B9E08E6A88 CRC64;
                                                                   of.
                                                                                                                                                                                                                                             B.;
vaccinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304
                                                                 mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 AA
                                                                   0f
                                                                                                                                                                                                                                             virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 352;
                                                                   vaccinia virus with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and the
                                                                                                                                                                                                                                             A-type inclusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  e. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
```

PIR; PIR;

```
DDCCCCCCCCCCCCCCCTTTTAXXOCCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orthopoxviruses.";
J. Gen. Virol. 74:1679-1684(1993).
J. Gen. Virol. 74:1679-1684(1993).
J. Gen. Virol. 74:1679-1684(1993).
J. Gen. Viruses.";
J. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 15
ATI_CAMPC
Q05482;
Q1-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepeah Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content used by non-profit institutions as long as its content used by non-profit institutions as long as its content used by non-profit institutions as long as its content used to be a long to the long to t
                                                                                                                    entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meyer H., Rziha H.-J.; "Characterization of the gene encoding the A-type inclusion protein of camelpox virus and sequence comparison with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
01-FEB-1995 (Rel. 31, Last annotation
A-TYPE INCLUSION PROTEIN (ATI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M61187; AAA48321.1; -.
EMBL; M76371; AAA48275.1; -.
EMBL; X57318; CAA40574.1; -.
PIR; A41701; WMV224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Camelpox virus (strain CP-1).
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 93346980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 KRRNVEWELS-RLRRDIKECDK-YKEDLDKAK 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MATURE VIRUSES ARE OCCLUDED INTO THE ATI, AND IT HAS BEEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING DISSEMINATION FROM ANIMAL TO AN INFECT OF ATI IS THE FORMATION MISCELLANEOUS: A CHARACTERISTIC FEATURE OF ATI IS THE FORMATION LARGE MASSES WITH NO SURROUNDING MEMBRANES IN THE CYTOPLASM OF INFECTED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                 DISSEMINATION FROM ANIMAL TO ANIMAL.
MISCELLANEOUS: A CHARACTERISTIC FEATURE OF
LARGE MASSES WITH NO SURROUNDING MEMBRANES
INFECTED CELLS.
302162; J
322022; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN N-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: 92% IDENTITY TO COWPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRQCMQLETSGQMRRCVSQCDKRFEEDIDWSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 40.6%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WMVZ94.
S29908.
587 58
610 61
618 6
682 6
724 AA;
JQ2162.
S32022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          588
618
682
                                                                                                                                                            license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84235 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQ -> SK (IN REF. 3).
R -> H (IN REF. 3).
R -> RR (IN REF. 3).
S -> R (IN REF. 3).
S -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.39e
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73; DB 1; I
No. 1.39e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą
                                                                                                                                                        http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                  ATI IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INCLUSION
                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                                                                                                                                                              THE FORMATION OF CYTOPLASM OF
                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                       EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPLASM OF
                                                                                                                                                                                                                                                                                          a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                          commercial
                                                                                                                                                                                                                                                         on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   얶
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٧,
```

一日 中国大学大学は大学の

```
KW Late protein: Repeat:
FT GOMAIN 609 719 4 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 609 636 1.
FT REPEAT 637 664 2.
FT REPEAT 685 688 3.
FT REPEAT 689 719 4.
SQ SEQUENCE 726 AA; 84415 MW; 1DB20A175C786F20 CRC64;
Query Match 20.2%; Score 73; DB 1; Length 726;
Best Local Similarity 40.6%; Pred. No. 1.39e+00;
Matches 13; Conservative 10; Mismatches 7; Indels 2; Gaps 2;
Db 551 KRRNVEWELS-RLRRDIKECDK-YKEDLDKAK 580
||: :: | | :: | | :: | | : | | : | | | | | | |
Qy 40 KRQCMQLETSGQMRRCVSQCDKRFEEDIDMSK 71

Search completed: Sat May 13 09:25:11 2000
Job time : 92 secs.
```

